Multilocus sequence typing (MLST) of *Helicobacter suis*

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A multilocus sequence typing (MLST) scheme was developed for *Helicobacter suis* (*H. suis*). This bacterium is considered to be one of the risk factors associated with gastric ulcers in pigs and is also of zoonotic significance[2]. Recently *H. suis* has been successfully cultured *in vitro*[1] and genome annotations of two isolates have been completed. The genetic diversity in 9 isolates, all obtained from the stomach of pigs, was studied by examination of allelic variation in 7 housekeeping genes *atpA, efp, mutY, ppa, trpC, ureI, vhpC* by MLST. These genes have also been used in the MLST scheme of *Helicobacter pylori*[3]. The *ppa* gene showed 100% homogeneity among the 9 isolates and does not seem to be useful in a MLST scheme for *H. suis*. Results obtained with the 6 other genes showed that the different isolates belonged to different sequence types, indicating that the present MLST scheme shows enough discriminatory power. MLST may be applied for strain typing directly in tissue samples and may allow to determine whether certain genotypes are more often associated with gastric disease in pigs and humans than other genotypes.

1. Baele et.al., 2008. Int. J. Syst. Evol. Microbiol. 58, 1350-1358.
2. Haesebrouck et. al., 2009. Clin. Microbiol. Rev. 22, 202-223.
3. *Helicobacter pylori* Multilocus Sequence Typing website (http://pubmlst.org/helicobacter)